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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:28:04 / Search time 166 Seconds
(without alignments)
62.907 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59
Perfect score: 27
Sequence: 1 FFAVANGNELLDLSLTVMNTEPERT 27

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980a:*
2: geneseqp1990a:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003b:*
8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	90	AA51476	Aa51476 Human TRF
2	27	100.0	90	AA28938	Aab28938 T cell re
3	27	100.0	90	AA87679	Aay87679 Feline hu
4	27	100.0	92	AA51475	Aa51475 Human TRF
5	27	100.0	92	AA28937	Aab28937 T cell re
6	27	100.0	92	AA87678	Aay87678 Feline hu
7	27	100.0	97	AA12123	Aar12123 TRFP chat
8	27	100.0	97	AA51472	Aa51472 Human TRF
9	27	100.0	97	AA28935	Aab28935 T cell re
10	27	100.0	97	AA90105	Aay90105 Cat TRFP
11	27	100.0	97	AA87675	Aay87675 Feline hu
12	27	100.0	100	AD038397	Ad038397 Cat aller
13	27	100.0	107	AD62496	Ad62496 Cat aller
14	27	100.0	109	AA12122	Aar12122 TRFP I ch
15	27	100.0	109	AA41985	Aa41985 Human T c
16	27	100.0	109	AA36541	Aar36541 TRFP chat
17	27	100.0	109	AA25593	Aay25593 Fells sp.
18	27	100.0	109	AA51471	Aa51471 Human TRF
19	27	100.0	109	AA28934	Aab28934 T cell re
20	27	100.0	109	AA90104	Aay90104 Cat TRFP
21	27	100.0	109	AA87674	Aay87674 Feline hu
22	27	100.0	109	AD03483	Ad03483 Cat aller
23	27	100.0	109	AD12179	Ad12179 Cat aller
24	27	100.0	110	AA27370	Aar27370 TRFP chat
25	27	100.0	111	AA12121	Aar12121 TRFP chat

ALIGNMENTS

26	27	100.0	111	2	AA27359	Aar27359 TRFP Chat
27	27	100.0	111	3	AA51470	Aa51470 Human TRF
28	27	100.0	111	3	AA28933	Aab28933 T cell re
29	27	100.0	111	3	AA90103	Aay90103 Cat TRFP
30	27	100.0	111	3	AA87673	Aay87673 Feline hu
31	26	96.3	26	2	AA41977	Aa41977 Human T c
32	26	96.3	26	2	AA36544	Aar36544 Peptide Z
33	26	96.3	26	3	AA51481	Aa51481 Human TRF
34	26	96.3	26	3	AA28943	Aab28943 Peptide Z
35	26	96.3	26	3	AA90109	Aay90109 Cat TRFP
36	26	96.3	26	3	AA87684	Aay87684 Feline hu
37	26	96.3	96	2	AA36548	Aar36548 Recombito
38	26	96.3	96	3	AA28979	Aab28979 Peptide Y
39	26	96.3	96	3	AA90145	Aay90145 TRFP fusi
40	19	70.4	82	3	AA51478	Aa51478 Human TRF
41	19	70.4	82	3	AA28940	Aab28940 T cell re
42	19	70.4	82	3	AA90106	Aay90106 Cat TRFP
43	19	70.4	82	3	AA87681	Aay87681 Feline hu
44	19	70.4	101	2	AA27372	Aar27372 TRFP Chat
45	18	66.7	18	3	AA51487	Aa51487 Human TRF

RESULT 1
AA51476
ID AA51476 standard; protein; 90 AA.
XX
AC AA51476;
XX
DT 22-MAY-2000 (first entry)
XX
DE Human TRFP chain 2 (short form) protein fragment #2.
XX
KW T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
KM down regulation; immune response; allergen; immunoglobulin E;
KW sensitivity; cat protein allergen; human; chain 2.
XX
OS Homo sapiens.
XX
PN US6019972-A.
XX
PD 01-FEB-2000.
XX
PF 02-SEP-1994; 94US-00300928.
XX
PR 03-NOV-1989; 89US-00431565.
PR 28-FEB-1991; 91US-00662276.
PR 13-DEC-1991; 91US-00807529.
PR 25-MAR-1992; 92US-00857311.
PR 15-MAY-1992; 92US-00884718.
PR 15-JAN-1993; 93US-00006116.
XX
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
PI Garman RD, Greenstein JL, Kuo M, Briner TV, Morville M;
PI Gelfer ML;
XX
XX WPI, 2000-146862/13.
XX
DR Peptides of human T cell reactive feline protein for treating sensitivity
XX to cat protein allergens comprise at least one T cell epitope recognized
PT by a T cell receptor specific for the human T cell reactive feline
PT protein.
XX
PS Example 1; Col 83-84; 105pp; English.
XX
CC This invention describes a novel peptide (I) of human T cell reactive
CC feline protein (hTRFP) having at least one T cell epitope recognized by a
CC T cell receptor specific for the human T cell reactive feline protein,
CC the peptide consisting of at least 7-30 amino acids, and having an amino
CC acid sequence derived from an amino acid sequence comprising 94, 96, 97,

CC 109, or 111 residues, given in the specification. The peptides down
 CC regulate the immune response to the allergen. The peptides have reduced
 CC immunoglobulin E binding and reduce T cell responsiveness. The peptide
 CC (I) is useful in compositions for treating sensitivity to a cat protein
 CC allergen in a subject. This sequence represents the human TRFP chain 2
 CC (short form)

XX Sequence 90 AA;

Query Match 100.0%; Score 27; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.9e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLDLSLTKNATEPERT 27
 DB 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 2

AAB28938
 ID AAB28938 standard; protein; 90 AA.

XX AAB28938;

XX 29-JAN-2001 (first entry)

XX T cell reactive feline protein chain 2 PRO short.

XX Cat; allergy; human T cell reactive feline protein; hTRFP; immunotherapy.

XX Felis sp.

XX US6120769-A.

XX 19-SEP-2000.

XX 28-APR-1995; 95US-00431184.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00061116.

XX 02-SEP-1994; 94US-00300928.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Gelfer ML, Garman RD, Greenstein JL, Bond JF;

XX WPI; 2000-601477/57.

XX Detecting, preventing and treating sensitivity to cat protein allergen

XX comprises combining a biological sample with a human T cell reactive

XX feline protein and determining the extent of binding that occurs.

XX Disclosure; Fig 7; 106pp; English.

XX The present invention relates to the detection of sensitivity to a cat

XX protein allergen by combining a blood sample from a subject with a

XX peptide of human T cell reactive feline protein (hTRFP). This method and

XX the hTRFP peptides are useful for diagnosing, preventing and treating cat

XX allergies by reducing or abolishing an individual's allergic response to

XX a cat allergen. DNA encoding the TRFP may be used as probes to locate

XX equivalent sequences present in other species. These may further be used

XX to study the mechanism of immunotherapy of cat allergy, and to design

XX modified derivatives, analogues or functional equivalents useful in

XX immunotherapy. The present sequence was used in the invention

XX Sequence 90 AA;

XX Query Match 100.0%; Score 27; DB 3; Length 90;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FFAVANGNELLDLSLTKNATEPERT 27
 DB 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 3

AAV87679
 ID AAV87679 standard; protein; 90 AA.

XX AAV87679;

XX 22-AUG-2000 (first entry)

XX Feline human TRFP chain 2 short form protein #2.

XX T-cell reactive feline protein; TRFP, Fel d I; cat allergen;

XX anti-allergic; T cell stimulator; diagnostic; immunotherapy.

XX Felis sp.

XX US6048962-A.

XX 11-APR-2000.

XX 27-APR-1995; 95US-00430014.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00061116.

XX 02-SEP-1994; 94US-00300928.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Kuo M, Rogers BL, Gelfer ML, Morgenstern JP, Brauer AW;

XX Greenstein JL, Griffith ID, Garman RD;

XX WPI; 2000-316905/27.

XX New human T cell reactive feline protein useful for reducing or

XX abolishing individual's allergic response to cat allergen comprising two

XX different covalently linked peptide chains.

XX Example 2; Col 83-84; 106pp; English.

XX This invention describes a novel naturally occurring cat protein allergen

XX (I), human T cell reactive feline protein (TRFP), comprising two

XX different covalently linked peptide chains with a molecular weight of 20

XX kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD

XX under reducing conditions. The products of the invention have

XX anti-allergic activity and act as human T cell stimulators. TRFP is useful

XX for reducing or preventing the adverse effects of cat allergens on cat

XX allergic individuals and in ex vivo diagnostic tests to determine which

XX cat peptides cause sensitivity so as to selectively use them to desensitize a

XX cat sensitive individual. Purified TRFP is also useful for studying the

XX mechanism of immunotherapy of cat allergy and to design modified

XX derivatives, analogs or functional equivalents that are more useful in

XX immunotherapy against cat allergy. DNA sequences encoding TRFP are useful

XX as probes to locate equivalent sequences present in other species (goats,

XX sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or

XX therapeutics. Fully defined and characterized TRFP provides complete and

XX a very simple desensitization therapy. This sequence represents a human T

XX cell reactive feline protein (also known as Fel d I) chain 2, short form

XX which is described in the method of the invention

XX Sequence 90 AA;

XX Query Match 100.0%; Score 27; DB 3; Length 90;

XX Best Local Similarity 100.0%; Pred. No. 2.9e-19;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
 |||||
 DB 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 4
 AAY51475
 ID AAY51475 standard; protein; 92 AA.
 XX

AC AAY51475;

XX 22-MAY-2000 (first entry)

XX Human TRFP chain 2 (long form) protein fragment #2.

XX T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;
 down regulation; immune response; allergen; immunoglobulin E;

XX sensitivity; cat protein allergen; human; chain 2.

XX Homo sapiens.

XX US6019972-A.

XX 01-FEB-2000.

XX 02-SEP-1994; 94US-00300928.

XX 03-NOV-1989; 89US-00431565.

XX 28-FEB-1991; 91US-00662276.

XX 13-DEC-1991; 91US-00807529.

XX 25-MAR-1992; 92US-00857311.

XX 15-MAY-1992; 92US-00884718.

XX 15-JAN-1993; 93US-00006116.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Garman RD, Greenstein JL, Kuo M, Briner TU, Morville M;

XX Geffer ML;

XX WPI; 2000-146862/13.

XX Peptides of human T cell reactive feline protein for treating sensitivity

XX to cat protein allergens comprise at least one T cell epitope recognized

XX by a T cell receptor specific for the human T cell reactive feline

XX protein.

XX Example 1; Col 83-84; 105pp; English.

XX This invention describes a novel peptide (1) of human T cell reactive

XX feline protein (hTRFP) having at least one T cell epitope recognized by a

XX T cell receptor specific for the human T cell reactive feline protein,

XX the peptide consisting of at least 7-30 amino acids, and having an amino

XX acid sequence derived from an amino acid sequence comprising 94, 96, 97,

XX 109, or 111 residues, given in the specification. The peptides down

XX regulate the immune response to the allergen. The peptides have reduced

XX immunoglobulin E binding and reduce T cell responsiveness. The peptide

XX (1) is useful in compositions for treating sensitivity to a cat protein

RESULT 5

AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

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AA28937

ID: AA28937 standard; protein; 92 AA.

[illegible]

XX	Felis catus.	
OS		
XX		
XX	Key	Location/Qualifiers
FT	Peptide	3..19
FT	Protein	/label= Leader sequence
FT		20..97
FT		/label= TRFP I truncated short form
XX		
PN	W09106571-A.	
XX		
PD	16-MAY-1991.	
XX		
PF	03-NOV-1989;	89US-00431565.
XX		
PR	03-NOV-1989;	89US-00431565.
XX		
PA	(IMMU-) IMMUNOLOGIC PHARM COR.	
XX		
PI	Gelfer MU, Garman RD, Greenstein JL, Juo M, Rogers BL, Brauer AW;	
DR	WPI; 1991-164136/22.	
DR	N-PSDB; AAQ11840.	
XX		
PT	New pure covalently linked human T cell reactive feline protein - and	
PT	modified peptide(s), used to reduce effects of cat allergens and to	
PT	diagnose sensitivity to allergens.	
XX		
PS	Claim 2; Fig 5; 70pp; English.	
XX		
CC	Poly-A mRNA from cat parotid and mandibular glands was used to produce	
CC	cDNA clones for both chain 1 and chain 2 of TRFP. These clones were then	
CC	used to screen a cat genomic library. Chain 1 exists in two forms having	
CC	different leader sequences (A and B). The sequence can be used to express	
CC	the protein and peptide derive. which stimulate T-cells in persons	
CC	allergic to cats. The peptides can be used to reduce/eliminate the	
CC	allergic response partic. by modifion. of lymphokine prodn. by the T-	
CC	cells. They can also be used to identify epitopes responsible for	
CC	sensitivity. The DNA can be used to detect comparable sequence in other	
CC	species, and also for prodn. of modified forms of TRFP esp. showing	
CC	reduced binding to IgE and thus reduced tendency to cause adverse	
CC	reactions. See also AARI2119-R12122	
XX		
SQ	Sequence 97 AA;	
	Query Match	100.0%; Score 27; DB 2; Length 97;
	Best Local Similarity	100.0%; Pred. No. 3.1e-19;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Cy	1 FFAVANGNELLDLSLRKVNATEPERT 27	
Db	33 FFAVANGNELLDLSLRKVNATEPERT 59	
	RESULT 8	
	AAVS1472	
ID	AAVS1472 standard; protein; 97 AA.	
XX		
AC	AAVS1472;	
XX		
DT	22-MAY-2000 (first entry)	
XX		
DE	Human TRFP chain 2 (truncated form) protein fragment.	
XX		
XX	T-cell reactive feline protein; TRFP; T cell epitope; T cell receptor;	
KW	down regulation; immune response; allergen; immunoglobulin G;	
KW	sensitivity; cat protein allergen; human; chain 2.	
XX		
OS	Homo sapiens.	
XX		
PN	US6019972-A.	
XX		
PD	01-FEB-2000.	

XX 02-SEP-1994; 94US-00300928.
 XX 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 92US-00006116.
 XX (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX Garman RD, Greenstein JL, Kuo M, Briner TV, Morville M;
 PI Gelfer ML;
 XX WPI; 2000-146862/13.
 DR N-PSDB; AA288619.
 XX Peptides of human T cell reactive feline protein for treating sensitivity
 PT to cat protein allergens comprise at least one T cell epitope recognized
 PT by a T cell receptor specific for the human T cell reactive feline
 PT protein.
 XX Claim 1; Col 81-82; 105pp; English.
 XX This invention describes a novel peptide (I) of human T cell reactive
 CC feline protein (hTRFP) having at least one T cell epitope recognized by a
 CC T cell receptor specific for the human T cell reactive feline protein,
 CC the peptide consisting of at least 7-30 amino acids, and having an amino
 CC acid sequence derived from an amino acid sequence comprising 94, 96, 97,
 CC 109, or 111 residues, given in the specification. The peptides down
 CC regulate the immune response to the allergen. The peptides have reduced
 CC immunoglobulin E binding and reduce T cell responsiveness. The peptide
 CC (I) is useful in compositions for treating sensitivity to a cat protein
 CC allergen in a subject. This sequence represents the human TRFP chain 2
 CC (truncated form)
 XX
 SQ Sequence 97 AA;
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PFAVANGNELLDLSTKVNATEPERT 27
 DB 33 PFAVANGNELLDLSTKVNATEPERT 59
 RESULT 9
 AAB28935
 ID AAB28935 standard; protein; 97 AA.
 XX
 AC AAB28935;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE T cell reactive feline protein chain 2 truncated form.
 XX
 KW Cat; allergy; human T cell reactive feline protein; hTRFP; immunotherapy.
 XX
 OS Felis sp.
 XX
 PN US6120769-A.
 XX
 PD 19-SEP-2000.
 XX
 PF 28-APR-1995; 95US-00431184.
 XX
 PR 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 92US-00006116.

PR 15-JAN-1993; 93US-00006116.
 PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX Garman RD, Greenstein JL, Bond JF;
 PI Gelfer ML;
 XX WPI; 2000-601477/57.
 DR N-PSDB; AAC60105.
 XX Detecting, preventing and treating sensitivity to cat protein allergen
 PT comprises combining a biological sample with a human T cell reactive
 PT feline protein and determining the extent of binding that occurs.
 XX
 PS Claim 1; Fig 5; 106pp; English.
 XX The present invention relates to the detection of sensitivity to a cat
 CC protein allergen by combining a blood sample from a subject with a
 CC peptide of human T cell reactive feline protein (hTRFP). This method and
 CC the hTRFP peptides are useful for diagnosing, preventing and treating cat
 CC allergies by reducing or abolishing an individual's allergic response to
 CC a cat allergen. DNA encoding the TRFP may be used as probes to locate
 CC equivalent sequences present in other species. These may further be used
 CC to study the mechanism of immunotherapy of cat allergy, and to design
 CC modified derivatives, analogues or functional equivalents useful in
 CC immunotherapy. The present sequence was used in the invention
 XX
 SQ Sequence 97 AA;
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PFAVANGNELLDLSTKVNATEPERT 27
 DB 33 PFAVANGNELLDLSTKVNATEPERT 59
 RESULT 10
 AAY90105
 ID AAY90105 standard; protein; 97 AA.
 XX
 AC AAY90105;
 XX
 DT 12-SEP-2003 (revised)
 DT 13-JUL-2000 (first entry)
 XX
 DE Cat TRFP chain 2 truncated form protein sequence.
 XX
 KW Cat; TRFP; human T-cell reactive feline protein; cat protein allergen;
 KW house dust; Fel d 1; cat allergy; feline domesticus sensitivity; therapy;
 KW diagnosis; goat; sheep; horse; rabbit; dog.
 XX
 OS Felis catub.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /note= "signal peptide"
 FT /note= "mature TRFP chain 2 truncated form"
 XX
 PN US6025162-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 28-APR-1995; 95US-00430944.
 XX
 PR 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.

PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Morgenstern JP, Griffith IJ, Rogers BL;
 XX WPI; 2000-181812/16.
 DR N-PSDB; AAA07439.
 XX
 PT New human T cell reactive feline protein, useful for desensitizing cat
 XX allergic individuals to cat allergens.
 PS Claim 1; Fig 5; 108pp; English.
 XX
 CC This sequence is a peptide chain of the human T cell reactive feline
 CC protein (TRFP) of the invention. The protein is a cat protein allergen,
 CC and was isolated from a vacuum bag extract obtained by affinity
 CC purification of house dust collected from several homes with cats. TRFP
 CC is composed of two covalently linked peptide chains, and is also referred
 CC to as Fel d 1. TRFP and its peptides are useful for reducing or
 CC preventing the adverse effects that exposure to cat allergens normally
 CC has on cat allergic individuals (i.e. to desensitize individuals to cat
 CC allergens or block the effect of the allergens). TRFP is also used in
 CC methods of diagnosing sensitivity to feline domesticus in an individual.
 CC DNA sequences encoding TRFP can be used as probes to locate equivalent
 CC sequences present in other species, e.g. goat, sheep, horse, rabbit and
 CC dog, that may be useful in a diagnostic and/or therapeutic applications.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 97 AA;
 XX
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PFAVANGNELLDLSTKVNATEPERT 27
 DB 33 PFAVANGNELLDLSTKVNATEPERT 59
 XX
 RESULT 11
 AA87675
 ID AAY87675 standard; protein; 97 AA.
 XX
 AC AAY87675;
 XX
 DT 22-AUG-2000 (first entry)
 XX
 DE Feline human TRFP chain 2 truncated form protein.
 XX
 KW T-cell reactive feline protein; TRFP; Fel d 1; cat allergen;
 KW anti-allergic; T cell stimulator; diagnostic; immunotherapy.
 XX
 OS Felle sp.
 XX
 PN US6048962-A.
 XX
 PD 11-APR-2000.
 XX
 PF 27-APR-1995; 95US-00430014.
 XX
 PR 03-NOV-1989; 89US-00431565.
 PR 28-FEB-1991; 91US-00662276.
 PR 13-DEC-1991; 91US-00807529.
 PR 25-MAR-1992; 92US-00857311.
 PR 15-MAY-1992; 92US-00884718.
 PR 15-JAN-1993; 93US-00006116.
 PR 02-SEP-1994; 94US-00300928.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Kuo M, Rogers BL, Gefter ML, Morgenstern JP, Brauer AW,
 PI Greenstein JL, Griffith IJ, Garman RD;

XX
 DR WPI; 2000-316905/27.
 DR N-PSDB; AAA12246.
 XX
 PT New human T cell reactive feline protein useful for reducing or
 PT abolishing individual's allergic response to cat allergen comprising two
 XX different covalently linked peptide chains.
 PS Claim 2; Col 79-80; 106pp; English.
 XX
 CC This invention describes a novel naturally occurring cat protein allergen
 CC (1), human T cell reactive feline protein (TRFP), comprising two
 CC different covalently linked peptide chains with a molecular weight of 20
 CC kD, 40 kD or 130 kD under non-reducing conditions and 5 kD or 10-18 kD
 CC under reducing conditions. The products of the invention have
 CC anti-allergic activity and act as human T cell stimulators. TRFP is useful
 CC for reducing or preventing the adverse effects of cat allergens on cat
 CC allergic individuals and in ex vivo diagnostic tests to determine which a
 CC peptides cause sensitivity so as to selectively use them to desensitize a
 CC cat sensitive individual. Purified TRFP is also useful for studying the
 CC mechanism of immunotherapy of cat allergy and to design modified
 CC derivatives, analogs or functional equivalents that are more useful in
 CC immunotherapy against cat allergy. DNA sequences encoding TRFP are useful
 CC as probes to locate equivalent sequences present in other species (goats,
 CC sheep, dogs, rabbits or horses) that may be useful in diagnostics and/or
 CC therapeutics. Fully defined and characterised TRFP provides complete and
 CC a very simple desensitization therapy. This sequence represents a human T
 CC cell reactive feline protein (also known as Fel d 1) chain 2, truncated
 CC form which is described in the method of the invention
 XX
 SQ Sequence 97 AA;
 XX
 Query Match 100.0%; Score 27; DB 3; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.1e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PFAVANGNELLDLSTKVNATEPERT 27
 DB 33 PFAVANGNELLDLSTKVNATEPERT 59
 XX
 RESULT 12
 ADO38397
 ID ADO38397 standard; peptide; 100 AA.
 XX
 AC ADO38397;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Cat allergen Fel d1 MHC class II-presented epitope #5.
 XX
 KW Antibacterial; Virucide; Antiparasitic; Antiarthritic;
 KW Antirheumatic; Neuroprotective; Antiinflammatory; Dermatological;
 KW Immunosuppressive; Antidiabetic; Antithyroid; Antiasbatic;
 KW Antiallergic; Cytostatic; Antipneumatic; Gene Therapy; Vaccine;
 KW MHC Class II; II-key motif; Immune response; anthrax; EBOLA; HIV;
 KW influenza; vaccinia virus; infection; bacterium; virus; parasite; fungus;
 KW rickettsia; rheumatoid arthritis; multiple sclerosis;
 KW lupus erythematosus; diabetes mellitus; myasthenia gravis;
 KW autoimmune thyroiditis; scleroderma; dermatomyositis; pemphigus; asthma;
 KW allergic rhinitis; topical dermatitis; colitis; cancer; psoriasis;
 KW adenoma; cat; cat dander; Fel d1.
 XX
 OS Felle catu.
 XX
 PN US2004058881-A1.
 XX
 PD 25-MAR-2004.
 XX
 PF 24-SEP-2002; 2002US-00253286.
 XX
 PR 24-SEP-2002; 2002US-00253286.
 XX

PA (ANTI-) ANTIGEN EXPRESS INC.
 XX
 PI Humphreys RE, Xu M;
 XX
 DR WPI; 2004-294259/27.
 XX
 PT New non-naturally occurring protein or polypeptide modified by .
 PT recombinant DNA techniques, useful for treating multiple sclerosis,
 PT diabetes mellitus, myasthenia gravis, scleroderma, allergic rhinitis,
 PT colitis, cancer or psoriasis.
 XX
 PS Example 4; Page 24; 90pp; English.
 XX
 CC The invention relates to a non-naturally occurring protein or polypeptide
 CC (1) modified by recombinant DNA techniques comprising: a C-terminal
 CC element comprising an MHC Class II-presented epitope; an N-terminal
 CC element comprising an Ii-key motif; and an intervening element comprising
 CC a sequence of 4-11 amino acid residues where the modification by
 CC recombinant DNA techniques taking place within elements (b) and (c). Also
 CC described are methods for: suppressing or enhancing an immune response
 CC directed toward an MHC (major histocompatibility complex) Class II-
 CC presented epitope of interest. Suppressing an immune response directed
 CC toward an MHC Class II-presented epitope of interest comprises: providing
 CC a nucleic acid sequence encoding the MHC Class II-presented epitope of
 CC interest, the nucleic acid sequence encoding an Ii-key motif located 4-11
 CC amino acids upstream from the N-terminal residue of the MHC Class II-
 CC presented epitope of interest; and modifying the Ii-key motif to decrease
 CC its conformance to the archetypal Ii-Key regulatory motif. Enhancing an
 CC immune response directed toward an MHC Class II-presented epitope of
 CC interest comprises: providing a nucleic acid sequence encoding the MHC
 CC Class II-presented epitope of interest, the nucleic acid sequence lacking
 CC an Ii-key motif located 4-11 amino acids upstream from the N-terminal
 CC residue of the MHC Class II-presented epitope of interest; and modifying
 CC the nucleic acid sequence to introduce an Ii-key motif appropriately
 CC spaced from the MHC Class II-presented epitope. The protein or
 CC polypeptide of interest corresponds to a protein or polypeptide encoded
 CC by an infectious pathogen selected from anthrax, EBOLA, HIV or influenza,
 CC preferably vaccinia virus. The non-naturally occurring protein or
 CC polypeptide (1) modified by recombinant DNA techniques is useful for
 CC treating infectious diseases caused or associated with infection by a
 CC bacterium, virus, parasite, fungus, rickettsia or other infectious
 CC agents. It is also useful for treating rheumatoid arthritis, multiple
 CC sclerosis, lupus erythematosus, diabetes mellitus, myasthenia gravis,
 CC autoimmune thyroiditis, scleroderma, dermatomyositis, pemphigus, asthma,
 CC allergic rhinitis, topical dermatitis, colitis, cancer, psoriasis or
 CC adenomas. The present sequence represents the amino acid sequence of a
 CC cat allergen Fel d1 chain 1 MHC class II-presented epitope used in the
 CC invention.
 CC
 XX
 SQ Sequence 100 AA;
 XX
 Query Match 100.0%; Score 27; DB 8; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.2e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PFAVANGNELLDLSITKVNATEPERT 27
 Db 31 PFAVANGNELLDLSITKVNATEPERT 57
 XX
 RESULT 13
 ADH62496
 ID ADH62496 standard; protein; 107 AA.
 XX
 AC ADH62496;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Cat allergen Fel d I (chain 2) protein.
 XX
 KW Allergen; vaccine; gene therapy; transgenic animal; Fel d I;
 KW embryonic stem cell; allergy; cat.
 XX

OS Felis catus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..17
 FT /label= Leader_Peptide
 FT Protein 18..107
 FT /note= "Mature Fel d I chain 2 protein"
 XX
 PN US2003177512-A1.
 XX
 PD 18-SEP-2003.
 PD
 PF 18-NOV-2002; 2002US-00295903.
 PF
 PR 13-JUN-1995; 95US-0000189P.
 PR 07-JUN-1996; 96US-0065790S.
 PR 11-JAN-1999; 99US-00227873.
 XX
 PA (AYNE/) AYNER D B.
 XX
 PI Ayner DB;
 XX
 DR WPI; 2003-898650/82.
 DR N-PSDB; ADH62495.
 XX
 PT New polynucleotide sequence encoding a disrupted Fel d I gene, useful for
 PT preparing a vaccine against allergy.
 XX
 PS Disclosure; SEQ ID NO 4; 25pp; English.
 XX
 CC The present invention relates to a method of producing transgenic cats
 CC wherein the gene sequences coding for major cat allergen Fel d I have
 CC been disrupted. The invention provides a polynucleotide sequence that
 CC encodes a disrupted Fel d I gene. The Fel d I gene has been disrupted by
 CC sequence alignment, sequence insertion or deletion of all or part of the
 CC Fel d I gene. It has been disrupted with a polynucleotide sequence
 CC encoding a selectable marker, which is a gene that confers neomycin
 CC resistance. The cat is heterozygous or homozygous for the disrupted Fel d
 CC I gene. It does not produce the cat allergen Fel d I. It is fertile and
 CC capable of transmitting the disrupted Fel d I gene to its offspring. The
 CC Fel d I gene of the somatic cells or germ line cells of the cat is
 CC disrupted. The method of the invention comprises introducing a cat stem
 CC cell comprising a disrupted Fel d I gene into a cat embryo, transplanting
 CC the embryo into a pseudopregnant cat, and allowing the cat embryo to
 CC mature into a cat. The method also comprises producing a first and second
 CC heterozygous transgenic cats, where the second cat is not the same sex as
 CC the first cat, breeding the first and second cats, and selecting
 CC transgenic cats that are homozygous for the disrupted Fel d I gene and do
 CC not produce Fel d I antigen. The polynucleotide sequence provided by the
 CC invention is useful for preparing a vaccine against allergy. The present
 CC sequence is cat Fel d I (chain 2) protein sequence.
 CC
 XX
 SQ Sequence 107 AA;
 XX
 Query Match 100.0%; Score 27; DB 7; Length 107;
 Best Local Similarity 100.0%; Pred. No. 3.4e-19;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 PFAVANGNELLDLSITKVNATEPERT 27
 Db 31 PFAVANGNELLDLSITKVNATEPERT 57
 XX
 RESULT 14
 AAR12122
 ID AAR12122 standard; protein; 109 AA.
 XX
 AC AAR12122;
 XX
 DT 26-JUL-1991 (first entry)
 XX
 DE TRFP I chain 2 - short form.
 XX

KW	Human T cell reactive feline protein; cat allergens.				
XX					
OS	Felis catus.				
XX					
FH	Key	Location/Qualifiers			
FT	Peptide	3..19			
FT		/label= Leader sequence			
FT	Protein	20..111			
XX		/label= TRFP I short form			
PM	W09106571-A.				
XX					
PD	16-MAY-1991.				
XX					
PF	03-NOV-1989;	89US-00431565.			
XX					
PR	03-NOV-1989;	89US-00431565.			
XX					
PA	(IMMU-) IMMUNOLOGIC PHARM COR.				
PI	Gelfer ML, Garman RD, Greenstein JL, Juo M, Rogers BL, Brauer AW;				
DR	MP1, 1991-164136/22.				
XX	N-PSDB; AAQ11839.				
PT	New pure covalently linked human T cell reactive feline protein - and				
PT	modified peptide(s), used to reduce effects of cat allergens and to				
PT	diagnose sensitivity to allergens.				
XX					
PS	Claim 2; Fig 4; 70pp; English.				
XX					
CC	Poly-A mRNA from cat parotid and mandibular glands was used to produce				
CC	cDNA clones for both chain 1 and chain 2 of TRFP. These clones were then				
CC	used to screen a cat genomic library. Chain 1 exists in two forms having				
CC	different leader sequences (A and B). The sequence can be used to express				
CC	the protein and peptide derivs. which stimulate T-cells in persons				
CC	allergic to cats. The peptides can be used to reduce/eliminate the				
CC	allergic response partic. by modifcn. of lymphokine prodn. by the T-				
CC	cells. They can also be used to identify epitopes responsible for				
CC	sensitivity. The DNA can be used to detect comparable sequence in other				
CC	species, and also for prodn. of modified forms of TRFP esp. showing				
CC	reduced binding to IgB and thus reduced tendency to cause adverse				
CC	reactions. See also AAR12119-R12123				
XX					
SQ	Sequence 109 AA;				
	Query Match 100.0%; Score 27; DB 2; Length 109;				
	Best Local Similarity 100.0%; Pred. No. 3.5e-19;				
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
QY	1 PFAVANGNELLDLSITKNATEPERT 27				
DB	33 PFAVANGNELLDLSITKNATEPERT 59				
RESULT 15					
AAR41985					
ID	AAR41985 standard; protein; 109 AA.				
XX					
AC	AAR41985;				
XX					
DT	25-MAR-2003 (revised)				
DT	21-APR-1994 (first entry)				
XX					
DE	Human T cell reactive feline protein chain 2.				
XX					
KW	Human; T cell; reactive; feline; protein; immune response; antigen;				
KW	tolerance; mammal; Dermatophagoides; Felis; Ambrosia; Lolium; Canis;				
KW	Cryptomeria; Alternaria; Alder; Betula; Quercus; Olea; Artemisia;				
XX	Plantago; Parietaria; Blatella; Apis; Periplaneta; autoantigen.				
XX					
OS	Homo sapiens.				
XX					

PH	Key	Location/Qualifiers
FT	Peptide	1..17
FT		/note= "Signal peptide"
FT	Protein	18..109
FT		/note= "Mature protein"
XX		
PN	WO9319178-A2.	
XX		
XD	30-SEP-1993.	
XX		
PF	25-MAR-1993;	93WO-US002462.
XX		
PR	25-MAR-1992;	92US-00857311.
PR	15-MAY-1992;	92US-00884718.
PR	15-JAN-1993;	93US-00006116.
PA	(IMMU-) IMMUNOLOGIC PHARM CORP.	
XX		
PI	Gelfer ML, Garman RD, Greenstein JL, Kuo M, Briner TV,	
PI	Morville M;	
XX		
DR	WPI; 1993-320744/40.	
DR	N-PSDB; AAQ49535.	
XX		
PT	New peptide(s) for inducing tolerance - comprise one or more epitope(s)	
PT	of an allergen administered subcutaneously, for treating sensitivity to	
PT	cats, bees, etc.	
XX		
PS	Disclosure; Fig 2; 107pp; English.	
XX		
CC	This sequence represents chain 2 of human T cell reactive feline protein	
CC	(TRFP). Peptides derived from TRFP may be used in a therapeutic	
CC	composition which is useful in treating diseases which involve an immune	
CC	response to a protein antigen. This composition may be used to induce	
CC	tolerance in a mammal to dermatophagides, Felis, Ambrosia, Lolium,	
CC	Cryptococcus, Alternaria, Alder, Betula, Quercus, Olea, Artemesia,	
CC	Plantago, Parietaria, Canis, Blactella, Apis, Periplaneta and to	
CC	autoantigens in humans. (Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 109 AA:	
	Query Match	100.0%; Score 27; DB 2; Length 109;
	Best Local Similarity	100.0%; Pred. No. 3.5e-19;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 FFAVANGNELLDLSLTKNATPEPT 27	
Db	31 FFAVANGNELLDLSLTKNATPEPT 57	

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Job time : 167 secs

Search completed: October 18, 2005, 13:44:17
Job time : 167 secs

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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:47:36 ; Search time 170 Seconds
(without alignments)
66.203 Million cell updates/sec

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Perfect score: 27
Sequence: 1 PFAVANGNELLDLSITKVNATEBERT 27

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 1660064 seqs, 416830855 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1660064

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*

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- 19: /cgn2_6/ptodata/2/pubppaa/US11_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	107	14	US-10-295-903-4
2	27	100.0	109	8	US-08-464-363-6
3	27	100.0	109	10	US-09-847-208-98
4	27	100.0	109	15	US-10-245-871-136
5	27	100.0	109	15	US-10-463-113-6
6	27	100.0	109	15	US-10-253-286-136
7	27	100.0	109	16	US-10-809-689-32
8	26	96.3	26	8	US-08-464-363-9
9	26	96.3	26	15	US-10-463-113-9
10	26	96.3	96	8	US-08-464-363-39
11	26	96.3	96	15	US-10-463-113-39

12	16	59.3	21	8	US-08-464-363-17	Sequence 17, Appl
13	16	59.3	21	15	US-10-463-113-17	Sequence 17, Appl
14	15	59.6	15	8	US-08-464-363-19	Sequence 19, Appl
15	15	55.6	15	15	US-10-463-113-19	Sequence 5, Appl1
16	14	51.9	92	16	US-10-809-689-5	Sequence 183, App
17	12	44.4	16	15	US-10-245-871-183	Sequence 13, Appl
18	12	44.4	16	16	US-10-253-286-183	Sequence 188, App
19	12	44.4	21	15	US-10-245-871-188	Sequence 188, App
20	12	44.4	21	15	US-10-253-286-188	Sequence 188, App
21	12	44.4	17	16	US-10-809-689-11	Sequence 171, App
22	10	37.0	9	15	US-10-245-871-171	Sequence 171, App
23	9	33.3	9	15	US-10-253-286-171	Sequence 181, App
24	9	33.3	14	15	US-10-245-871-181	Sequence 181, App
25	9	33.3	14	15	US-10-253-286-181	Sequence 181, App
26	9	33.3	16	16	US-10-809-689-12	Sequence 65, Appl
27	7	25.9	7	8	US-08-464-363-65	Sequence 65, Appl
28	7	25.9	7	15	US-10-463-113-65	Sequence 65, Appl
29	7	25.9	62	14	US-10-029-386-2938	Sequence 151766, A
30	7	25.9	79	15	US-10-424-599-151766	Sequence 199810, A
31	7	25.9	106	16	US-10-437-963-199810	Sequence 61756, A
32	7	25.9	110	15	US-10-425-114-61756	Sequence 66395, A
33	7	25.9	132	15	US-10-425-114-66395	Sequence 133298, A
34	7	25.9	151	16	US-10-437-963-133298	Sequence 212287, A
35	7	25.9	169	16	US-10-425-115-212287	Sequence 37074, A
36	7	25.9	203	16	US-10-767-701-37074	Sequence 304369, A
37	7	25.9	246	16	US-10-425-115-304369	Sequence 43856, A
38	7	25.9	254	16	US-10-767-701-43856	Sequence 59866, A
39	7	25.9	317	18	US-10-450-763-32298	Sequence 304368, A
40	7	25.9	352	15	US-10-282-1224-59866	Sequence 18374, A
41	7	25.9	385	16	US-10-425-115-304368	Sequence 133292, A
42	7	25.9	455	15	US-10-369-493-18374	Sequence 170216, A
43	7	25.9	749	16	US-10-437-963-133292	
44	7	25.9	990	16	US-10-437-963-170216	
45	7	25.9				

ALIGNMENTS

RESULT 1
US-10-295-903-4
; Sequence 4, Application US/10295903
; Publication No. US20030177512A1
GENERAL INFORMATION:
; APPLICANT: AVNER, David B.
; TITLE OF INVENTION: METHOD OF GENETICALLY ALTERING AND PRODUCING ALLERGY FREE CATS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/295,903
; FILING DATE: 18-JUN-1999
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,189
; FILING DATE: 09-JUN-1995
; APPLICATION NUMBER: US 08/657,905
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 09/227,873
; FILING DATE: 11-JAN-1999
ATTORNEY/AGENT INFORMATION:
; NAME: SIMKIN, Michele M.

REGISTRATION NUMBER: 34,717
REFERENCE/DOCKET NUMBER: 40065/105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-295-903-4

Query Match 100.0%; Score 27; DB 14; Length 107;
Best Local Similarity 100.0%; Pred. No. 6.4e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
DB 31 FFAVANGNELLDLSLTKNATEPERT 57

RESULT 2
US-08-464-363-6
Sequence 6, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garman, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahlive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION/DOCKET NUMBER: 36,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-363-6

Query Match 100.0%; Score 27; DB 8; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
DB 31 FFAVANGNELLDLSLTKNATEPERT 57

RESULT 3
US-09-847-208-98
Sequence 98, Application US/09847208
Publication No. US20030082190A1
GENERAL INFORMATION:
APPLICANT: Saxon, Andrew
APPLICANT: Zhang, Ke
APPLICANT: Zhu, Daocheng
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
TITLE OF INVENTION: 19E-MEDIATED ALLERGIC DISEASES
FILE REFERENCE: UC67,002A
CURRENT APPLICATION NUMBER: US/09/847,208
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 177
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 98
LENGTH: 109
TYPE: PRT
ORGANISM: Felis silvestris catus (Cat)
US-09-847-208-98

Query Match 100.0%; Score 27; DB 10; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
DB 31 FFAVANGNELLDLSLTKNATEPERT 57

RESULT 4
US-10-245-871-136
Sequence 136, Application US/10245871
Publication No. US20030235594A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2013
CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 136
LENGTH: 109
TYPE: PRT
ORGANISM: Felis domesticus
US-10-245-871-136

Query Match 100.0%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
DB 31 FFAVANGNELLDLSLTKNATEPERT 57

RESULT 5
US-10-463-113-6

```
Sequence 6, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Wei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-463-113-6

Query Match      100.0%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 6,5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSLTQVNAPEPT 27
DB      31 FFAVANGNELLDLSLTQVNAPEPT 57

RESULT 6
US-10-253-286-136
Sequence 136, Application US/10253286
Publication No. US20040058881A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: II-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
```

```
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 136
LENGTH: 109
TYPE: PRT
ORGANISM: Felis domesticus
US-10-253-286-136

Query Match      100.0%; Score 27; DB 15; Length 109;
Best Local Similarity 100.0%; Pred. No. 6,5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSLTQVNAPEPT 27
DB      31 FFAVANGNELLDLSLTQVNAPEPT 57

RESULT 7
US-10-809-689-32
Sequence 32, Application US/10809689
Publication No. US20040265342A1
GENERAL INFORMATION:
APPLICANT: Eric Potter Clarkson
TITLE OF INVENTION: Methods and compositions for desensitisation
FILE REFERENCE: 5538/1010
CURRENT APPLICATION NUMBER: US/10/809,689
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: PCT/GB99/00080
PRIOR FILING DATE: 1999-01-11
PRIOR APPLICATION NUMBER: GB/9800445.0
PRIOR FILING DATE: 1998-01-09
PRIOR APPLICATION NUMBER: GB/9820474.6
PRIOR FILING DATE: 1998-09-21
NUMBER OF SEQ ID NOS: 124
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32
LENGTH: 109
TYPE: PRT
ORGANISM: Felis catus
US-10-809-689-32

Query Match      100.0%; Score 27; DB 16; Length 109;
Best Local Similarity 100.0%; Pred. No. 6,5e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FFAVANGNELLDLSLTQVNAPEPT 27
DB      31 FFAVANGNELLDLSLTQVNAPEPT 57

RESULT 8
US-08-464-363-9
Sequence 9, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenstern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Wei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
```

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-363-9

Query Match 96.3%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPER 26
DB 1 FFAVANGNELLDLSLTKNATEPER 26

RESULT 9
US-10-463-113-9
Sequence 9, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565

FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 742-4214
TELEFAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-463-113-9

Query Match 96.3%; Score 26; DB 15; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPER 26
DB 1 FFAVANGNELLDLSLTKNATEPER 26

RESULT 10
US-08-464-363-39
Sequence 39, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-363-39

Query Match 96.3%; Score 26; DB 8; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPER 26
DB 44 FFAVANGNELLDLSLTKNATEPER 69

RESULT 11
US-10-463-113-39
Sequence 39, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield, LLP
STREET: 28 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/463,113
FILING DATE: 16-Jun-2003

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-463-113-39

Query Match 96.3%; Score 26; DB 15; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.1e-17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPER 26
DB 44 FFAVANGNELLDLSLTKNATEPER 69

RESULT 12

US-08-464-363-17
Sequence 17, Application US/08464363
Publication No. US20030035815A1
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm

TITLE OF INVENTION: RECOMBITOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,363
FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,529
FILING DATE: 13-DEC-1991
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989

ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-015CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-464-363-17

Query Match 59.3%; Score 16; DB 8; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLT 16
DB 6 FFAVANGNELLDLSLT 21

RESULT 13

US-10-463-113-17
Sequence 17, Application US/10463113
Publication No. US20040057959A1
GENERAL INFORMATION:

APPLICANT: Rogers, Bruce L.
Morgenshtern, Jay
Bond, Julian F.
Garman, Richard D.
Greenstein, Julia L.
Kuo, Mei-chang
Morville, Malcolm

```

; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,113
; FILING DATE: 16-Jun-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-463-113-17

Query Match          59.3%; Score 16; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PFAVANGNELLDLSL 16
Db      6 PFAVANGNELLDLSL 21

RESULT 14
US-08-464-363-19
; Sequence 19, Application US/08464363
; Publication No. US20030035815A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,363
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-015CN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-363-19

Query Match          55.6%; Score 15; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 LDLSITKYNATEPPER 26
Db      1 LDLSITKYNATEPPER 15

RESULT 15
US-10-463-113-19
; Sequence 19, Application US/10463113
; Publication No. US20040057959A1
; GENERAL INFORMATION:
; APPLICANT: Rogers, Bruce L.
; APPLICANT: Morgenstern, Jay
; APPLICANT: Bond, Julian F.
; APPLICANT: Garman, Richard D.
; APPLICANT: Greenstein, Julia L.
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Morville, Malcolm
; TITLE OF INVENTION: RECOMBITOPE PEPTIDES
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,113
; FILING DATE: 16-Jun-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,529
; FILING DATE: 13-DEC-1991
; APPLICATION NUMBER: US 07/662,276
; FILING DATE: 28-FEB-1991
; APPLICATION NUMBER: US 07/431,565
; FILING DATE: 03-NOV-1989
; ATTORNEY/AGENT INFORMATION:
```

```

? NAME: Amy E. Mandargouize
? REGISTRATION NUMBER: 36,207
? REFERENCE/DOCKET NUMBER: IM1-015CN
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 227-7400
? TELEFAX: (617) 742-4214
? INFORMATION FOR SEQ ID NO: 19:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-463-113-19

```

```

Query Match 55.6%; Score 15; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 LDLSLTNNATBBER 26
|||||
Db 1 LDLSLTNNATBBER 15

```

Search completed: October 18, 2005, 14:01:48
Job time : 179 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:28:53 ; Search time 178 Seconds

(without alignments)
77.675 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27

Sequence: 1 FFAVANGNELLDLSLTAVNATEBERT 27

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched:

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	109	1	PEL2_FELCA
2	8	29.6	509	2	O6R1B4
3	7	25.9	77	2	O9K6B9
4	7	25.9	100	2	O8K1B4
5	7	25.9	106	2	O6ZDG2
6	7	25.9	134	2	O6PYC6
7	7	25.9	134	2	O6DMV1
8	7	25.9	198	2	O9X302
9	7	25.9	250	1	BACR_HAUS4
10	7	25.9	255	2	O6FCV6
11	7	25.9	273	2	O6CPS8
12	7	25.9	279	2	P738B5
13	7	25.9	303	2	O64761
14	7	25.9	310	2	O8KXR1
15	7	25.9	310	2	O6EXX1
16	7	25.9	310	2	O74P16
17	7	25.9	315	2	O8A9W0
18	7	25.9	320	1	ALX_PHOIL
19	7	25.9	322	2	O8LTP9
20	7	25.9	322	2	O9AAV5
21	7	25.9	358	2	O7MA28
22	7	25.9	420	1	HIS2_STNP7
23	7	25.9	428	2	O6CUA1
24	7	25.9	434	2	O7XQ04
25	7	25.9	455	2	O9CHP3
26	7	25.9	502	2	O84ZD1
27	7	25.9	524	2	O09012
28	7	25.9	524	2	O7SW4
29	7	25.9	525	2	O6VMU4
30	7	25.9	525	2	O6VMU5
31	7	25.9	525	2	O6VMU6

ALIGNMENTS

32	7	25.9	539	2	O6FV10
33	7	25.9	552	2	O6FQW2
34	7	25.9	1595	2	O7UG94
35	7	25.9	1601	2	O8IC14
36	6	22.2	23	2	O9H4H9
37	6	22.2	64	2	O8H5D6
38	6	22.2	86	2	O73910
39	6	22.2	86	2	O73911
40	6	22.2	86	2	O73912
41	6	22.2	87	2	O9PD8
42	6	22.2	88	2	O6Q214
43	6	22.2	91	2	O9LRB3
44	6	22.2	96	2	O8EUV5
45	6	22.2	97	2	O9FVJ7

RESULT 1
PEL2_FELCA STANDARD; PRT: 109 AA.

AC P30440;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B) (Fel d 1-B) (Allergen Cat-1) (Ag4) (Fdi).
GN Name=CH2;
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butirata; Carnivora; Fissipedia; Felidae; Fells.
NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-100.
RX MEDLINE=92052157; PubMed=1946388;
RA Morgenstern J.P., Griffith I.J., Brauer A.W., Rogers B.L., Bond J.F., Chapman M.D., Kuo M.-C.;
RT "Amino acid sequence of Fel d1, the major allergen of the domestic cat: protein sequence analysis and cDNA cloning."
RL Proc. Natl. Acad. Sci. U.S.A. 88:9690-9694(1991).
RN [2]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.
RC TISSUE=Liver;
RX MEDLINE=92241678; PubMed=1572548; DOI=10.1016/0378-1119(92)90405-E;
RA Griffith I.J., Craig S., Pollock J., Yu X.-B., Morgenstern J.P., Rogers B.L.;
RT "Expression and genomic structure of the genes encoding Fdi, the major allergen from the domestic cat."
RL Gene 113:263-268(1992).
RN [3]
RP SEQUENCE OF 18-37, AND CHARACTERIZATION.
RX MEDLINE=91287714; PubMed=1712068; DOI=10.1016/0161-5890(91)90141-6;
RA Duffort O.A., Carreira J., Nicli G., Polo F., Lombardero M.;
RT "Studies on the biochemical structure of the major cat allergen Fells domesticus I."
RL Mol. Immunol. 28:301-309(1991).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=84265679; PubMed=6747135;
RA Leternan K., Ohman J.L. Jr.;
RT "Cat allergen 1: biochemical, antigenic, and allergenic properties."
J. Allergy Clin. Immunol. 74:147-153(1984).
CC -1- SUBUNIT: Heterotetramer composed of two non-covalently linked disulfide-linked heterodimer of chains 1 and 2.
CC -1- ALTERNATIVE PRODUCTS:
CC Comment=Alternative splicing; Named isoforms=3;
CC isoforms:
CC Name=1; Synonyms=CH2L;
CC IsoId=P30440-1; Sequence=Displayed;
CC Name=2; Synonyms=CH2S;
CC IsoId=P30440-2; Sequence=VSP_004249;

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CC Name=3; Synonyms=CH2ST, Truncated;
CC Irida-P30440-3; Sequence=VSP 004248;
CC TISSUE SPECIFICITY: The long form is preferentially expressed in
CC the salivary gland, while the short form is preferentially
CC expressed in the skin.
CC -1- ALLERGEN: Causes an allergic reaction in human. Major allergen
CC produced by the domestic cat.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
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DR EMBL; M77341; AAC41616.1; -;
DR EMBL; X62478; CAA44345.1; -;
DR PIR; B53283; B53283.
DR PIR; C56413; C56413.
DR PIR; JCI127; JCI127.
DR InterPro; IPR006038; Uteroglobin supf.
KM Allergen: Alternative splicing; Direct protein sequencing;
KM Glycoprotein; Polymorphism; Signal.
FT FT SIGNAL 1 17
FT CHAIN 18 109 Major allergen I polypeptide chain 2.
FT CARBOHYD 50 50 N-linked (GlcNAc... )
FT VARSPLIC 82 109 TRISSKDCMGKAVQNTVDLKLNTLGR -> PSTNIAMVK
FT FT QTRTP (in isoform 3).
FT FT /FTIDA_VSP_004248.
FT FT /FTIDSVSP -> IAINFY (in isoform 2).
FT FT /FTIDSVSP 004249.
FT FT I -> L (in CH2SV).
FT FT I -> V (in CH2SV).
FT FT *VARIANT 72 72 RV -> KF (in CH2SV).
FT FT *VARIANT 74 75 M -> T (in CH2SV).
FT FT *VARIANT 91 91 Q -> E (in CH2SV).
FT FT *VARIANT 96 96 N -> K (in CH2SV).
FT FT *VARIANT 105 105 C -> F (in Ref. 3).
FT FT *VARIANT 24 24 F -> T (in Ref. 3).
FT FT *VARIANT 32 32
FT FT *VARIANT 109 AA; 11854 MM; 857FB9CD76036CB9 CRC64;
SQ SEQUENCE 109 AA; 11854 MM; 857FB9CD76036CB9 CRC64;

Query Match 100.0%; Score 27; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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ID 06R184 PRELIMINARY; PRT; 509 AA.
AC 06R184;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE FARI1 protein (Fragment).
GN Name=FARI1;
OS Zygoasaccharomyces rouxii (Candida mogii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Zygoasaccharomycetes.
OX NCB1_TaxID=956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 732;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY496963; AAR88365.1; -;
FT NON TER 509 509
SQ SEQUENCE 509 AA; 58713 MM; BAB6F2FB4E901589 CRC64;

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Query Match 29.6%; Score 8; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 7 GNEILLDL 14
DB 54 GNEILLDL 61

RESULT 3

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ID 09KG69 PRELIMINARY; PRT; 77 AA.
AC 09KG69;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE BH0244 protein.
GN Ordered locus names=BH0244;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCB1_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RL Nucleic Acids Res. 28:4317-4331 (2000).
DR EMBL; AP001507; BAB03963.1; -;
DR PIR; D83680; D83680.
KM Complete proteome.
SQ SEQUENCE 77 AA; 9511 MM; F9BEC3529F5CE320 CRC64;

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Query Match 25.9%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 9 ELLDL 15
DB 24 ELLDL 30

RESULT 4

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ID 08KLB4 PRELIMINARY; PRT; 100 AA.
AC 08KLB4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein yh014.
GN Name=yh014;
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCB1_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=91193195; PubMed=2013564;
RA Girard M.L., Flores M., Brom S., Romero D., Palacios R., Davila G.;
RT "Structural complexity of the symbiotic plasmid of Rhizobium
RT leguminosarum bv. phaseoli."
RL J. Bacteriol. 173:2411-2419 (1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN42;
RX MEDLINE=97419521; PubMed=9274036;
RA Ramirez-Romero M.A., Bustos P., Girard L., Rodriguez O.,
RA Cevallos M.A., Davila G.;

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"sequence, localization and characteristics of the replicator region of the symbiotic plasmid of *Rhizobium etli*.";
 RT Microbiology 143:2825-2831(1997).
 (3)
 RN SEQUENCE FROM N.A.
 RC STRAIN=CFN42;
 RX MEDLINE=22309397; PubMed=12421308;
 RA Quintero V., Cevallos M.A., Davila G.;
 RT "A site-specific recombinase (RinD) is required to exert incompatibility towards the symbiotic plasmid of *Rhizobium etli*.";
 RL Mol. Microbiol. 46:1023-1032(2002).
 (4)
 RN SEQUENCE FROM N.A.
 RP STRAIN=CFN42;
 RC Ramirez M.A., Bustos P., Girard L., Rodriguez O., Cevallos M.A., Davila G.;
 RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 (5)
 RN SEQUENCE FROM N.A.
 RP STRAIN=CFN42;
 RC Quintero V., Bustos P., Davila G.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 (6)
 RN SEQUENCE FROM N.A.
 RP STRAIN=CFN42;
 RC Gonzalez V., Bustos P., Medrano-Soto A., Ramirez-Romero M.A., Romero D., Salgado H., Hernandez-Gonzalez I., Hernandez-Celis J.C., Quintero V., Girard L., Rodriguez O., Flores M., Cevallos M.A., Collado-Vides J., Davila G.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 (7)
 RN SEQUENCE FROM N.A.
 RP STRAIN=CFN42;
 RC Quintero V., Bustos P., Davila G.;
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U80928; AAM54832.1; -;
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 100 AA; 11433 MW; 6179AB83270F7F4B CRC64;
 QY
 Db 10 LLLDLSL 16
 |||||
 84 LLLDLSL 90
 Query Match 25.9%; Score 7; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 Q6ZDG2 PRELIMINARY; PRT; 106 AA.
 AC Q6ZDG2;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein P0451G12.25 (Hypothetical protein OJ111.B05.3).
 DE OJ111.B05.3).
 GN Name=P0451G12.25; Synonyms=OJ111.B05.3;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrharioideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 (2)
 RN SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004139; BAD09348.1; -;
 DR EMBL; AP004154; BAD09194.1; -;

KW Hypothetical protein.
 SQ SEQUENCE 106 AA; 10471 MW; 1152A36A14B66D80 CRC64;
 QY
 Db 3 AVANGNE 9
 |||||
 31 AVANGNE 37
 Query Match 25.9%; Score 7; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 Q6PYC6 PRELIMINARY; PRT; 134 AA.
 AC Q6PYC6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Bacteriorhodopsin (Fragment).
 GN Name=bop;
 OS Natrinema ajinwuenis.
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Natrinema.
 OC NCBI_TaxID=222984;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=AJ12, AJ13, and AJ11;
 RA Xu X.W., Wu M.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY570920; AAS87572.1; -;
 DR EMBL; AY570921; AAS87573.1; -;
 DR EMBL; AY570919; AAS87571.1; -;
 DR HSP; P02945; 1KG9.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR InterPro; IPR001425; Bac_rhodopsin.
 DR Pfam; PF01036; Bac_rhodopsin; 1.
 DR PRINTS; PR00251; BACTERIAL_OPSIN.
 DR PROSITE; PS00327; BACTERIAL_OPSIN_RET; 1.
 FT NON_TER 1
 FT NON_TER 134
 SQ SEQUENCE 134 AA; 14303 MW; 86A51BC6DAFAC CRC64;
 QY
 Db 10 LLLDLSL 16
 |||||
 3 LLLDLSL 9
 Query Match 25.9%; Score 7; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 Q6DMV1 PRELIMINARY; PRT; 134 AA.
 AC Q6DMV1;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2812A;
 RX MEDLINE=22839765; PubMed=12959402; DOI=10.1089/1076629032286445;
 RA Santagati M., Iannelli F., Cascone C., Campanile F., Oggioni M.R., Stefani S., Pozzi G.;
 RT "The novel conjugative transposon Tn1207.3 carries the macroide

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RT efflux gene mef(A) in Streptococcus pyogenes.";
RL Microb. Drug Resist. 9:243-247(2003).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=2812A;
RA Santegati M., Iannelli F., Cascone C., Stefani S., Pozzi G.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF657002; AAT72374.1; -.
KW Hypothetical protein.
SQ SEQUENCE 134 AA; 15373 MW; 897916A18372A242 CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 2; Length 134;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLDLSLT 17
DB 25 LLDLSLT 31

RESULT 8
Q9X302 PRELIMINARY; PRT; 198 AA.
ID Q9X302;
AC 09X302;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE PX01-31.
OS Bacillus anthracis.
OC Plasmid virulence plasmid PX01.
OC Bacteri; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=1392;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne;
RX MEDLINE=99445483; PubMed=10515943;
RA Okinaka R.T., Cloud K., Hampton O., Hofmeister A.R., Hill K.K.,
RA Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
RA Martinez Y., Rieke D., Svensson R., Jackson P.J.;
RT "Sequence and organization of px01, the large Bacillus anthracis
RT plasmid harboring the anthrax toxin genes.";
RL J. Bacteriol. 181:6509-6515(1999).
RW EMBL; AF065404; AAD3235.1; -.
DR FIR; G59094; G59094.
KW Plasmid.
SQ SEQUENCE 198 AA; 22859 MW; D76737FD81C43C9D CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 2; Length 198;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NEILLDL 14
DB 150 NEILLDL 156

RESULT 9
BACR HALS4 STANDARD; PRT; 250 AA.
ID BACR HALS4;
AC 093740;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bacteriorhodopsin (BR).
GN Name=brp;
OS Halobacterium sp. (strain arg-4).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxId=160432;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=99096913; PubMed=878396; DOI=10.1006/jmbi.1998.2286;
RT Ihara K., Umemura T., Katagiri I., Kitajima-Ihara T., Sugiyama Y.,

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RA Kimura Y., Mukohata Y.;
RT "Evolution of the archael rhodopsins: evolution rate changes by gene
RT duplication and functional differentiation.";
RL J. Mol. Biol. 285:163-174(1999).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=2812A;
RA Santegati M., Iannelli F., Cascone C., Stefani S., Pozzi G.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF657002; AAT72374.1; -.
KW Hypothetical protein.
SQ SEQUENCE 134 AA; 15373 MW; 897916A18372A242 CRC64;

Query Match
Best Local Similarity 25.9%; Score 7; DB 2; Length 250;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLDLSL 16
DB 101 LLDLSL 107

RESULT 10
Q6FCV6 PRELIMINARY; PRT; 255 AA.
ID Q6FCV6;
AC Q6FCV6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Survival protein (Acid phosphatase) (EC 3.1.3.2).
GN Name=surv; OrderedLocNames=ACTAD1227;
OS Actinobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Actinobacter.
OX NCBI_TaxId=62977;
RN (1)
RP SEQUENCE FROM N.A.
RX Barbe V., Vallonet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Criveller S., Robert C., Duprat S., Winkler P.,
RA Ornston L.N., Weisenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Actinobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";

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RL Nucleic Acids Res. 0:0-0(2004).
 DR EMBL; CR543861; CAG68103.1; -.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.
 DR InterPro; IPR002828; SURF.
 DR Pfam; PF01975; SURF.1.
 DR ProDom; PD005378; SURF.1.
 DR TrIRPfam; TIGR00087; SURF.1.
 KM Complete proteome.
 SQ SEQUENCE 255 AA; 27574 MW; C4EB04235E82A46 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FAVANG 7
 DB 224 FAVANG 230

RESULT 11
 ID 06CP58 PRELIMINARY; PRT; 273 AA.
 AC 06CP58;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to sp|P26754|Saccharomyces cerevisiae YNL312w RFA2 DNA replication factor A.
 GN ORFNames=KLLA0B0734Bg;
 OS Kluyveromyces lactis NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_Taxid=284590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E., Goffard N., Frangul L., Aigle M., Anthouard V., Bahour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Catolico L., Confiantoli F., de Daruvar A., Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A., Hantave F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B., Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J., Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-1140;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; C3382125; CAG9368.1; -.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR008994; Nucleic_acid_OB.
 DR InterPro; IPR004365; tRNA anti.
 DR Pfam; PF01336; tRNA anti.1.
 SQ SEQUENCE 273 AA; 30347 MW; 4121F346314942BD CRC64;

Query Match 25.9%; Score 7; DB 2; Length 273;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FAVANG 8
 DB 174 FAVANG 180

RESULT 12
 ID P73885 PRELIMINARY; PRT; 279 AA.
 AC P73885;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE S1R0267 protein.
 GN OrderedLocName=s1r0267;
 OS Synchocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
 NCBI_Taxid=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kikura T., Hosouchi T., Matsuo A., Muraki A., Nakazaki N., Nario K., Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90910; BAA17949.1; -.
 DR PIR; S75087; S75087.
 DR HSP; 031743; 1PUV.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR005289; GTP-binding.
 DR InterPro; IPR006073; GTP_OBG.
 DR InterPro; IPR002917; MMR_HSR1.
 DR Pfam; PF01926; MMR_HSR1.1.
 DR PRINTS; PR00326; GTP_OBG.
 DR TrIRPfam; TIGR00650; MG442.1.
 SQ SEQUENCE 279 AA; 31201 MW; 9AA60F3118D77763 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDLSL 16
 DB 213 LLLDLSL 219

RESULT 13
 ID 064761 PRELIMINARY; PRT; 303 AA.
 AC 064761;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative phosphatidylinositol-glycan synthase.
 GN Name=At2g34980;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R., Venter J.C.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004238; AAC12837.1; -.

DR PIR; T00479; T00479.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0017176; F:phosphatidylinositol N-acetylglucosaminyltr. . .; IEA.
 DR GO; GO:0006506; P:GPI anchor biosynthesis; IEA.
 DR InterPro; IPR009450; GPI2.
 DR Pfam; PF06432; GPI2; 1.
 SQ SEQUENCE 303 AA; 34200 MW; 8856BF82F4940C92 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLLDLSL 16
 |||||
 DB 89 NLLDLSL 95

RESULT 14

OKXRI PRELIMINARY; PRT; 310 AA.
 ID Q8KXR1
 AC Q8KXR1; 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein BXA0045.
 GN Name=BXA0045;
 OS Bacillus anthracis str. A2012.
 OG Plasmid PX01.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_TaxID=191218;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A2012;
 RC MEDLINE=22061436; PubMed=12004073; DOI=10.1126/science.1071837;
 RA Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
 RA Holtzapfel E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
 RA Keim P., Fraser C.M.;
 RT "Comparative Genome Sequencing for Discovery of Novel Polymorphisms in
 RT Bacillus anthracis.";
 RT Science 296:2028-2033(2002).
 DR EMBL; AE011190; AAM26001.1; -.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 310 AA; 36423 MW; 716F21DB64CFE274 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NLLDLSL 14
 |||||
 DB 262 NLLDLSL 268

RESULT 15

Q6EZK1 PRELIMINARY; PRT; 310 AA.
 ID Q6EZK1
 AC Q6EZK1; 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=GBAA_PX01_0045;
 OS Bacillus anthracis.
 OG Plasmid PX01.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_TaxID=1392;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ames / Isolate 0581;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics.";

RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE017336; AAT28786.2; -.
 DR TIGR; GBAA_PX01_0045; -.
 KW Complete proteome.
 SQ SEQUENCE 310 AA; 36423 MW; 716F21DB64CFE274 CRC64;

Query Match 25.9%; Score 7; DB 2; Length 310;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NLLDLSL 14
 |||||
 DB 262 NLLDLSL 268

Search completed: October 18, 2005, 13:47:25
 Job time : 182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:37:20 ; Search time 39 Seconds
(without alignments)
66.612 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27
Sequence: 1 FFAVANGNELLDLSITKVATEPERT 27

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	107	2 JC1127	major allergen cha
2	27	100.0	109	2 C56413	major allergen Fel
3	27	100.0	77	2 D83680	hypothetical prote
4	7	25.9	198	2 C59094	hypothetical prote
5	7	25.9	250	2 T50677	bacteriorhodopsin
6	7	25.9	279	2 S75087	hypothetical prote
7	7	25.9	303	2 T00479	probable phosphati
8	7	25.9	455	2 B86722	biotin carboxylase
9	7	25.9	524	2 S44982	flagellin - Shigel
10	6	22.2	87	2 B82678	hypothetical prote
11	6	22.2	100	2 B90093	hypothetical prote
12	6	22.2	106	1 K1RTA	Ig kappa chain C r
13	6	22.2	107	2 D22598	hypothetical prote
14	6	22.2	112	2 T09060	hypothetical prote
15	6	22.2	118	2 H90453	hypothetical prote
16	6	22.2	127	2 A33894	choistmate mutase
17	6	22.2	147	2 A32066	hypothetical prote
18	6	22.2	150	2 P97303	transcription regu
19	6	22.2	155	2 I45913	interleukin-2 prec
20	6	22.2	155	2 S11468	interleukin-2 prec
21	6	22.2	160	2 T33995	hypothetical prote
22	6	22.2	161	2 G86541	CT260 hypothetical
23	6	22.2	161	2 H72082	conserved hypotet
24	6	22.2	170	2 H72039	dihydrofolate redu
25	6	22.2	170	2 B86585	conserved hypotet
26	6	22.2	174	2 F81741	degenerate transpo
27	6	22.2	175	2 B97974	Holliday junction
28	6	22.2	191	2 C72411	phosphoglycerate m
29	6	22.2	199	2 H87416	

30	6	22.2	201	2 S76151	hypothetical prote
31	6	22.2	210	1 ISVKRL	phosphoribosylanth
32	6	22.2	226	2 T30615	hypothetical prote
33	6	22.2	227	2 D71312	probable Holliday
34	6	22.2	229	2 S57957	thrombospondin 1 -
35	6	22.2	230	2 UN0060	hypothetical 24.5K
36	6	22.2	237	2 D83969	RNA polymerase spo
37	6	22.2	237	2 F70606	probable prtmF spo
38	6	22.2	238	2 H95105	pillin gene inverti
39	6	22.2	239	2 B39441	transcription init
40	6	22.2	239	1 U00083	transcription init
41	6	22.2	240	2 S75462	hypothetical prote
42	6	22.2	240	2 T20791	hypothetical prote
43	6	22.2	246	2 S19193	hypothetical prote
44	6	22.2	246	2 T20792	hypothetical prote
45	6	22.2	249	2 AH2152	hypothetical prote

ALIGNMENTS

RESULT 1

JC1127

major allergen chain 2 precursor, short form - cat

C:Species: Felis silvestris catus (domestic cat)

C:Date: 31-Dec-1993 #sequence_rev1sion 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: JC1127

R:Griffith, I.J.; Craig, S.; Pollock, J.; Yu, X.B.; Morgenstern, J.P.; Rogers, B.L.

Gene 113, 263-268, 1992

A:Title: Expression and genomic structure of the genes encoding Fd1, the major allergen

A:Reference number: JC1126; MUID:92241678; PMID:1572548

A:Accession: JC1127

A:Molecule type: DNA

A:Residues: 1-107 <GRL>

A:Cross-references: UNIPROT:P30440; GB:X62478; NID:9395406; PIDN:CAA44345.1; PID:9395407

A:Experimental source: skin

C:Genetics:

A:Gene: Ch2

A:Introns: 21/1; 81/3

C:Keywords: glycoprotein

F:1-17/Domain: signal sequence #status predicted <SIG>

F:18-107/Product: major allergen chain 2, short form #status predicted <MNT>

F:50/Banding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVATEPERT 27

DB 31 FFAVANGNELLDLSITKVATEPERT 57

RESULT 2

C56413

major allergen Fel di chain 2 precursor - cat

C:Species: Felis silvestris catus (domestic cat)

C:Date: 11-Aug-1995 #sequence_rev1sion 11-Aug-1995 #text_change 09-Jul-2004

C:Accession: C56413; JC1145

R:Morgenstern, J.P.; Griffith, I.J.; Brauer, A.W.; Rogers, B.L.; Bond, J.F.; Chapman, M

Proc. Natl. Acad. Sci. U.S.A. 88, 9690-9694, 1991

A:Title: Amino acid sequence of Fel d1, the major allergen of the domestic cat: protein

A:Reference number: A56413; MUID:92052157; PMID:1946388

A:Accession: C56413

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-109 <MOR>

A:Cross-references: UNIPROT:P30440; GB:M77341; NID:9163822; PIDN:AA41616.1; PID:9163823

R:Griffith, I.J.; Craig, S.; Pollock, J.; Yu, X.B.; Morgenstern, J.P.; Rogers, B.L.

Gene 113, 263-268, 1992

A:Title: Expression and genomic structure of the genes encoding Fd1, the major allergen

A:Reference number: JC1126; MUID:92241678; PMID:1572548

A:Accession: JC1145

A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 18-109 <GR>
A:Experimental source: salivary gland
C:Keywords: glycoprotein
F:1-1//Domain: signal sequence #status predicted <Sig>
F:50/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 27; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
|||||
DB 31 FFAVANGNELLDLSITKVNATEPERT 57

RESULT 3

DB3680
hypothetical protein BH0244 [imported] - *Bacillus halodurans* (strain C-125)
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: D83680

R:Takami, H.; Nakaone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeni, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A:Reference number: AB3650; MUID:20512582; PMID:11058132

A:Accession: D83680
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <STO>
A:Cross-references: UNIPROT:Q9KG69; GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA8039
A:Experimental source: strain C-125
C:Genetics:

A:Gene: BH0244

Query Match 25.9%; Score 7; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ELLLDLS 15
|||||
DB 24 ELLLDLS 30

RESULT 4

GS9094
hypothetical protein pX01-31 - *Bacillus anthracis* virulence plasmid pX01
C:Species: *Bacillus anthracis*
C>Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C:Accession: G59094

R:Okimura, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
J. Bacteriol. 181, 6509-6515, 1999
A>Title: Sequence and organization of pX01, the large *Bacillus anthracis* plasmid harbored
A:Reference number: A55091; MUID:99445463; PMID:10515943

A:Accession: G59094
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-198 <OKI>
A:Cross-references: UNIPROT:Q9X302; GB:AF065404; NID:G4694216; PIDN:AAD3235.1; PID:G469
A:Experimental source: strain Sterne
C:Genetics:

A:Gene: pX01-31

A:Genome: plasmid

Query Match 25.9%; Score 7; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NELLDL 14
|||||
DB 150 NELLDL 156

RESULT 5
TS0677
bacteriorhodopsin [similarity] - "*Haloterrigena*" sp. (strain arg-4)
C:Species: "*Haloterrigena*" sp.
A:Variety: strain arg-4
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000
C:Accession: T50677

R:Iihara, K.; Umemura, T.; Katagiri, I.; Kitajima-Iihara, T.; Sugiyama, Y.; Kimura, Y.; Mu
J. Mol. Biol. 285, 163-174, 1999
A>Title: Evolution of the archaeal rhodopsins: Evolution rate changes by gene duplicatio
A:Reference number: Z2703; MUID:99096913; PMID:9878396

A:Accession: T50677
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-250 <IHA>

A:Cross-references: EMBL:AB009620; PIDN:BA75200.1
C:Genetics:

A:Gene: bop
C:Superfamily: bacteriorhodopsin
C:Keywords: chromoprotein; photoreceptor; retinal; transmembrane protein
F:225/Binding site: retinal (Lys) (covalent) #status predicted

Query Match 25.9%; Score 7; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDLSL 16
|||||
DB 101 LLLDLSL 107

RESULT 6

S75087
hypothetical protein slr0267 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S75087
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
B.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75087
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-279 <KAN>
A:Cross-references: UNIPROT:P73685; EMBL:D90910; GB:AB001339; NID:G1652956; PIDN:BA1794
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: conserved hypothetical protein MG442

Query Match 25.9%; Score 7; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDLSL 16
|||||
DB 213 LLLDLSL 219

RESULT 7

T00479
probable phosphatidylinositol-glycan synthase [imported] - *Arabidopsis thaliana*
N:Alternate names: hypothetical protein F1913.21
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C:Accession: T00479; B84763
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, April 1998
A:Description: *Arabidopsis thaliana* chromosome II BAC F1913 genomic sequence.

A:Reference number: Z14160
 A:Accession: T00479
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-303 <RCU>
 A:Cross-references: UNIPROT:064761; EMBL:AC004238; NID:G3033373; PID:G3033393
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:1061197
 A:Accession: B84763
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-303 <STO>
 A:Cross-references: GB:AE002093; NID:G3033393; PIDN:AA012837.1; GSPDB:GN00139
 A:Genetics:
 A:Gene: ATG34980; F1913.21
 A:Map position: 2

Query Match 25.9%; Score 7; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LLLDLSL 16
 |||||
 DB 89 LLLDLSL 95

RESULT 8
 B86722
 biotin carboxylase (EC 6.3.4.14) [imported] - Lactococcus lactis subsp. lactis (strain I
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B86722
 R:Bohlooin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: B86722
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-455 <STO>
 A:Cross-references: UNIPROT:Q9CHF3; GB:AE005176; PID:G12723697; PIDN:AAK04876.1; GSPDB:G
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: accC
 C:Superfamily: biotin carboxylase, biotin carboxylase homology
 C:Keywords: ligase

Query Match 25.9%; Score 7; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VANGNEL 10
 |||||
 DB 316 VANGNEL 322

RESULT 9
 S44982
 flagellin - *Shigella sonnei*
 C:Species: *Shigella sonnei*
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S44982; S44981
 R:Tomimaga, A.; Mahmoud, M.A.H.; Mukaihara, T.; Enomoto, M.
 Mol. Microbiol. 12, 277-285, 1994
 A:Title: Molecular characterization of intact, but cryptic, flagellin genes in the genus
 A:Reference number: S44980; MUID:94335647; PMID:8057852
 A:Accession: S44982
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-524 <TOM>
 A:Cross-references: UNIPROT:Q09012; EMBL:D16821; NID:G391893; PIDN:BA04095.1; PID:G39185
 C:Superfamily: Flagellin

Query Match 25.9%; Score 7; DB 2; Length 524;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LTVNAT 22
 |||||
 DB 196 LTVNAT 202

RESULT 10
 B82678
 hypothetical protein XF1461 [imported] - *Xylella fastidiosa* (strain 945c)
 C:Species: *Xylella fastidiosa*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: B82678
 R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: B82678
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-87 <SIM>
 A:Cross-references: UNIPROT:Q9PDB8; GB:AE003976; GB:AE003849; NID:G9106479; PIDN:AAE9427
 A:Experimental source: strain 945c
 A:Authors: Ferreira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 R.; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.; A
 Britons, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H
 as-Neco, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miraca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tuhako, M.H.; Vallada, H.; Van Sluyt, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 A:Genetics:
 A:Gene: XF1461

Query Match 22.2%; Score 6; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 NELLLD 13
 |||||
 DB 2 NELLLD 7

RESULT 11
 E90093
 hypothetical protein orf100 [imported] - *Gulliardia theta* nucleomorph
 C:Species: nucleomorph *Gulliardia theta*
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: E90093
 R:Douglas, S.; Zauner, S.; Frumholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
 Nature 410, 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: E90093
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-100 <DOU>
 A:Cross-references: UNIPROT:Q98R80; GB:AF165818; NID:G13794502; PIDN:AAK39877.1; GSPDB G

C:Genetics:
A:Gene: orf100
A:Map position: 1
A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 22.2%; Score 6; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LLLDLS 15
DB 40 LLLDLS 45

RESULT 12

KIRTA
Ig kappa chain C region (allele a) - rat

C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Aug-1982 #sequence_revision 10-Sep-1982 #text_change 09-Jul-2004

C:Accession: A02118
R:Sheppard, H.W.; Gutman, G.A.
Proc. Natl. Acad. Sci. U.S.A. 78, 7064-7068, 1981

A:Title: Allelic forms of rat kappa chain genes: evidence for strong selection at the 1e
A:Reference number: A93901; M01D:82082587; PMID:6273508

A:Accession: A02118
A:Molecule type: DNA

A:Residues: 1-106 <SHE>
A:Cross-references: UNIPROT:P01836; GB:J02574; GB:J00745; NID:g204820; P1DN:AAA41411.1;

A:Experimental source: strain DA
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotrimer
F:19-88/Domains: immunoglobulin homology <IMM>

F:26-86/Domains: heterotrimer predicted
F:106/Domains: Interchain (to heavy chain) #status predicted

Query Match 22.2%; Score 6; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 LSLTKV 19
DB 71 LSLTKV 76

RESULT 13

D72598
Hypothetical protein APE1252 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: D72598
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; M01D:99310339; PMID:10382966
A:Accession: D72598

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-107 <RAM>
A:Cross-references: UNIPROT:Q9YCK5; DDBJ:AF000061; NID:95104821; P1DN:BAA80242.1; P1D:dl

A:Experimental source: strain K1
C:Genetics:

A:Gene: APE1252

Query Match 22.2%; Score 6; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 NATEPE 25
|||||

DB 84 NATEPE 89

RESULT 14

T09060
Hypothetical protein NG1 - mouse

C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09060
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc

submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: Z16543
A:Accession: T09060

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

A:Residues: 1-112 <ROW>
A:Cross-references: UNIPROT:O35443; EMBL:AF030001; NID:g2564945; PID:g2564948

C:Genetics:
A:Gene: NG1
A:Map position: 17

A:Introns: 13/3; 67/3

Query Match 22.2%; Score 6; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ELLDLD 14
DB 15 ELLDLD 20

RESULT 15

H90453
Hypothetical protein SS02777 [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: H90453
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A9139

A:Accession: H90453
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-118 <KUD>

A:Cross-references: UNIPROT:Q97V58; GB:AE006641; NID:g13816114; P1DN:AAK42887.1; GSPDB:G

C:Genetics:
A:Gene: SS02777

Query Match 22.2%; Score 6; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GNEELL 12
DB 21 GNEELL 26

Search completed: October 18, 2005, 13:48:10
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 18, 2005, 13:38:43 ; Search time 42 Seconds
(without alignments)
47,989 Million cell updates/sec

Title: US-09-662-784-6_COPY_33_59

Perfect score: 27

Sequence: 1 FFAVANGNELLDLSLTKNATEPERT 27

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	90	3 US-08-300-928C-14	Sequence 14, Appl
2	27	100.0	90	3 US-08-430-944D-14	Sequence 14, Appl
3	27	100.0	90	3 US-08-430-014-14	Sequence 14, Appl
4	27	100.0	90	3 US-08-431-184-14	Sequence 14, Appl
5	27	100.0	92	3 US-08-300-928C-13	Sequence 13, Appl
6	27	100.0	92	3 US-08-430-944D-13	Sequence 13, Appl
7	27	100.0	92	3 US-08-430-014-13	Sequence 13, Appl
8	27	100.0	92	3 US-08-431-184-13	Sequence 13, Appl
9	27	100.0	97	3 US-08-300-928C-10	Sequence 10, Appl
10	27	100.0	97	3 US-08-430-944D-10	Sequence 10, Appl
11	27	100.0	97	3 US-08-430-014-10	Sequence 10, Appl
12	27	100.0	97	3 US-08-431-184-10	Sequence 10, Appl
13	27	100.0	109	1 US-07-662-193-5	Sequence 5, Appl
14	27	100.0	109	1 US-07-807-529A-6	Sequence 6, Appl
15	27	100.0	109	3 US-08-300-928C-8	Sequence 8, Appl
16	27	100.0	109	3 US-08-430-944D-8	Sequence 8, Appl
17	27	100.0	109	3 US-08-430-014-8	Sequence 8, Appl
18	27	100.0	109	3 US-08-431-184-8	Sequence 8, Appl
19	27	100.0	109	5 PCT-US93-02462-6	Sequence 6, Appl
20	27	100.0	111	1 US-07-662-193-4	Sequence 4, Appl
21	27	100.0	111	3 US-08-300-928C-6	Sequence 6, Appl
22	27	100.0	111	3 US-08-430-944D-6	Sequence 6, Appl
23	27	100.0	111	3 US-08-430-014-6	Sequence 6, Appl
24	27	100.0	111	3 US-08-431-184-6	Sequence 6, Appl
25	26	96.3	26	1 US-07-807-529A-9	Sequence 9, Appl
26	26	96.3	26	3 US-08-300-928C-19	Sequence 19, Appl
27	26	96.3	26	3 US-08-430-944D-19	Sequence 19, Appl

28	26	96.3	26	3 US-08-430-014-19	Sequence 19, Appl
29	26	96.3	26	3 US-08-431-184-19	Sequence 19, Appl
30	26	96.3	26	5 PCT-US93-02462-9	Sequence 9, Appl
31	26	96.3	96	1 US-07-807-529A-39	Sequence 39, Appl
32	26	96.3	96	3 US-08-430-944D-103	Sequence 103, App
33	26	96.3	96	3 US-08-431-184-103	Sequence 103, App
34	26	96.3	96	3 US-08-300-928C-16	Sequence 16, Appl
35	19	70.4	82	3 US-08-430-944D-16	Sequence 16, Appl
36	19	70.4	82	3 US-08-430-014-16	Sequence 16, Appl
37	19	70.4	82	3 US-08-431-184-16	Sequence 16, Appl
38	19	70.4	83	1 US-07-662-193-7	Sequence 7, Appl
39	19	70.4	83	1 US-07-662-193-8	Sequence 8, Appl
40	18	66.7	18	3 US-08-300-928C-25	Sequence 25, Appl
41	18	66.7	18	3 US-08-430-944D-25	Sequence 25, Appl
42	18	66.7	18	3 US-08-430-014-25	Sequence 25, Appl
43	18	66.7	18	3 US-08-431-184-25	Sequence 25, Appl
44	18	66.7	27	3 US-08-300-928C-57	Sequence 57, Appl
45	18	66.7	27	3 US-08-430-944D-57	Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-08-300-928C-14
Sequence 14, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEPTER, Malcolm J., et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-14
Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFAVANGNELLDLSLTKNATEPERT 27

Db 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 2

US-08-430-944D-14
Sequence 14, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-14

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
Db 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 3
US-08-430-014-14
Sequence 14, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts

COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-014-14

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
Db 14 FFAVANGNELLDLSLTKNATEPERT 40

RESULT 4
US-08-431-184-14
Sequence 14, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-431-184-14

Query Match 100.0%; Score 27; DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 5
US-08-300-928C-13
Sequence 13, Application US/08300928C
Patent No. 6019972
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002,6US (IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-300-928C-13

Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
14 FFAVANGNELLDLSITKVNATEPERT 27

DB 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 6
US-08-430-944D-13
Sequence 13, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-430-944D-13

Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 7
US-08-430-014-13
Sequence 13, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA

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; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,014
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/300,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-08-430-014-13
Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
DB 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 8
US-08-431-184-13
; Sequence 13, Application US/08431184
; Patent No. 6120769
; GENERAL INFORMATION:
; APPLICANT: Bruce L. Rogers et al.
; TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,184
; FILING DATE: 28-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,014
; FILING DATE: 27-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,928
; FILING DATE: 02-SEPT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-044DV3
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```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 92 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
;
US-08-431-184-13
Query Match 100.0%; Score 27; DB 3; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
DB 14 FFAVANGNELLDLSITKVNATEPERT 40

RESULT 9
US-08-300-928C-10
; Sequence 10, Application US/08300928C
; Patent No. 6019772
; GENERAL INFORMATION:
; APPLICANT: GEFFER, Malcolm L. et al.
; TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,928C
; FILING DATE: September 2, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,529
; FILING DATE: December 13, 1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: AMY E. MANDRAGOURAS
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: 002.6US (IMI-044)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 97 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-300-928C-10
Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSITKVNATEPERT 27
DB 33 FFAVANGNELLDLSITKVNATEPERT 59
```

RESULT 10
US-08-430-944D-10
Sequence 10, Application US/08430944D
Patent No. 6025162
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,944D
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-430-944D-10
Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFAVANGNELLDLSLTKNATEPERT 27
DB 33 FFAVANGNELLDLSLTKNATEPERT 59
RESULT 11
US-08-430-014-10
Sequence 10, Application US/08430014
Patent No. 6048962
GENERAL INFORMATION:
APPLICANT: GERTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/300,928
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US(IMI-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
TELEFAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-430-014-10
Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FFAVANGNELLDLSLTKNATEPERT 27
DB 33 FFAVANGNELLDLSLTKNATEPERT 59
RESULT 12
US-08-431-184-10
Sequence 10, Application US/08431184
Patent No. 6120769
GENERAL INFORMATION:
APPLICANT: Bruce L. Rogers et al.
TITLE OF INVENTION: A HUMAN T CELL REACTIVE FELINE PROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHYE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,184
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,014
FILING DATE: 27-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,928
FILING DATE: 02-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-044DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-431-184-10

Query Match 100.0%; Score 27; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
|||||
Db 33 FFAVANGNELLDLSLTKNATEPERT 59

RESULT 13
US-07-662-193-5
Sequence 5, Application US/07662193

PATENT No. 5328991
GENERAL INFORMATION:
APPLICANT: Kuo, Mei-chang
APPLICANT: Bond, Julian
TITLE OF INVENTION: Improved Preparation of Cat Dander
TITLE OF INVENTION: Allergens for Immunotherapeutic Purposes and Uses Thereof
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/662,193
FILING DATE: 19910228
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991

ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: P36,207
REFERENCE/DOCKET NUMBER: IML89-02AA/IPC-002CC/INT-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

US-07-662-193-5

Query Match 100.0%; Score 27; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
|||||
Db 33 FFAVANGNELLDLSLTKNATEPERT 59

RESULT 14
US-07-807-529A-6
Sequence 6, Application US/07807529A

PATENT No. 5547669
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce L.
APPLICANT: Morgenstern, Jay
APPLICANT: Bond, Julian F.
APPLICANT: Garmen, Richard D.
APPLICANT: Greenstein, Julia L.
APPLICANT: Kuo, Mei-chang
APPLICANT: Morville, Malcolm
TITLE OF INVENTION: RECOMBIOPE PEPTIDES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: One Kendall Square, Building 600
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,529A
FILING DATE: 19911213
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,276
FILING DATE: 28-FEB-1991

APPLICATION NUMBER: US 07/431,565
FILING DATE: 03-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Channing, Stacey L.
REGISTRATION NUMBER: 31,095
REFERENCE/DOCKET NUMBER: IPC-027/4ml-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 494-0060
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-807-529A-6

Query Match 100.0%; Score 27; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNATEPERT 27
|||||
Db 31 FFAVANGNELLDLSLTKNATEPERT 57

RESULT 15
US-08-300-928C-8

Sequence 8, Application US/08300928C
PATENT No. 6019972

GENERAL INFORMATION:
APPLICANT: GEFTER, Malcolm L. et al.
TITLE OF INVENTION: PEPTIDES FOR HUMAN T CELL REACTIVE FELINE
TITLE OF INVENTION: PROTEIN (TRFP)
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: Massachusetts
COUNTRY: USA
ZIP: 02145

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,928C
FILING DATE: September 2, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,529
FILING DATE: December 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AMY E. MANDRAGOURAS
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: 002.6US (INT-044)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-300-928C-8

Query Match 100.0%; Score 27; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 3e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFAVANGNELLDLSLTKNVATEPERT 27
Db 33 FFAVANGNELLDLSLTKNVATEPERT 59

Search completed: October 18, 2005, 13:48:56
Job time: 43 secs

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